

Method	BLASTX
NCBI GI	g3914442
BLAST score	419
E value	2.0e-41
Match length	105
% identity	79
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.	163396
Seq. ID	LIB3177-062-P1-K1-E11
Method	BLASTX
NCBI GI	g3136033
BLAST score	183
E value	2.0e-13
Match length	87
% identity	44
NCBI Description	(AL023590) putative metallopeptidase [Schizosaccharomyces pombe]
Seq. No.	163397
Seq. ID	LIB3177-062-P1-K1-E12
Method	BLASTX
NCBI GI	g3915823
BLAST score	300
E value	1.0e-27
Match length	57
% identity	100
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5
Seq. No.	163398
Seq. ID	LIB3177-062-P1-K1-E2
Method	BLASTX
NCBI GI	g2493144
BLAST score	191
E value	1.0e-14
Match length	58
% identity	71
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.	163399
Seq. ID	LIB3177-062-P1-K1-E3
Method	BLASTX
NCBI GI	g4512685
BLAST score	469
E value	9.0e-64
Match length	155
% identity	79
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]


```
Seq. ID      LIB3177-062-P1-K1-G9
Method       BLASTX
NCBI GI      g3096931
BLAST score  576
E value      1.0e-59
Match length 113
% identity   99
NCBI Description (AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]
```

Seq. No.	163427
Seq. ID	LIB3177-062-P1-K1-H10
Method	BLASTN
NCBI GI	g2281081
BLAST score	227
E value	1.0e-125
Match length	227
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163428
Seq. ID	LIB3177-062-P1-K1-H11
Method	BLASTN
NCBI GI	g2351062
BLAST score	210
E value	1.0e-114
Match length	362
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163429
Seq. ID      LIB3177-062-P1-K1-H2
Method       BLASTX
NCBI GI      g2199574
BLAST score   340
E value      2.0e-32
Match length  65
% identity    98
NCBI Description (AF004293) aquaporin [Brassica rapa]
```

```
Seq. No.      163430
Seq. ID      LIB3177-062-P1-K1-H3
Method       BLASTX
NCBI GI      g3914658
BLAST score   294
E value      5.0e-27
Match length  74
% identity    80
NCBI Description  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
                >gi_1694974_emb_CAA70851_(Y09635) plastid ribosomal
                protein [Arabidopsis thaliana]
```

```
Seq. No.      163431
Seq. ID      LIB3177-062-P1-K1-H4
Method      BLASTX
```

```

NCBI GI          g2506443
BLAST score      553
E value          6.0e-57
Match length     139
% identity        78
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_2117520_pir_JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]

```

```
Seq. No.      163432
Seq. ID      LIB3177-062-P1-K1-H5
Method       BLASTX
NCBI GI      g113026
BLAST score   372
E value      9.0e-63
Match length  135
% identity    87
NCBI Description  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
>gi_68211_pir_WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
isocitrate lyase [Brassica napus]
```

Seq. No.	163433
Seq. ID	LIB3177-062-P1-K1-H6
Method	BLASTX
NCBI GI	g4741952
BLAST score	98
E value	8.0e-66
Match length	125
% identity	60
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

```
Seq. No.      163434
Seq. ID      LIB3177-062-P1-K1-H7
Method       BLASTX
NCBI GI      g132090
BLAST score   618
E value      2.0e-64
Match length  113
% identity    99
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir_RKMUB1
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700-
                (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                thaliana]
```

Seq. No. 163435


```
Seq. No.      163440
Seq. ID      LIB3177-063-P1-K1-A6
Method       BLASTX
NCBI GI      g3892722
BLAST score   534
E value      1.0e-54
Match length  120
% identity    92
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163441
Seq. ID      LIB3177-063-P1-K1-A7
Method       BLASTX
NCBI GI      g121075
BLAST score   259
E value      5.0e-23
Match length  63
% identity    84
NCBI Description  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725
(M82921) H-Protein precursor [Arabidopsis thaliana]
>gi_861215 (U27144) glycine decarboxylase complex H-protein
precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
glycine decarboxylase complex H-protein [Arabidopsis
thaliana] >gi_445119_prf_1908425A Gly
decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
```

```
Seq. No.      163442
Seq. ID      LIB3177-063-P1-K1-B1
Method       BLASTX
NCBI GI      g115385
BLAST score   216
E value      5.0e-18
Match length  43
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
```

Seq. No.	163443
Seq. ID	LIB3177-063-P1-K1-B11
Method	BLASTN
NCBI GI	g4455262
BLAST score	97
E value	2.0e-47
Match length	217
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

```
Seq. No.      163444
Seq. ID      LIB3177-063-P1-K1-B12
Method       BLASTX
NCBI GI      g4587564
BLAST score   364
E value      1.0e-72
Match length  145
```


% identity	68
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence
Seq. No.	163455
Seq. ID	LIB3177-063-P1-K1-C5
Method	BLASTN
NCBI GI	g4733953
BLAST score	138
E value	1.0e-71
Match length	285
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F13011 genomic sequence, complete sequence
Seq. No.	163456
Seq. ID	LIB3177-063-P1-K1-C6
Method	BLASTX
NCBI GI	g1488604
BLAST score	147
E value	2.0e-09
Match length	36
% identity	86
NCBI Description	(Z49842) ribulosebiphosphate carboxylase [Hordeum lechleri]
Seq. No.	163457
Seq. ID	LIB3177-063-P1-K1-C7
Method	BLASTN
NCBI GI	g4757405
BLAST score	154
E value	3.0e-81
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence
Seq. No.	163458
Seq. ID	LIB3177-063-P1-K1-C8
Method	BLASTN
NCBI GI	g3046849
BLAST score	209
E value	1.0e-114
Match length	213
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.	163459
Seq. ID	LIB3177-063-P1-K1-C9
Method	BLASTX
NCBI GI	g1170939
BLAST score	687
E value	1.0e-72
Match length	139
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)


```

BLAST score      53
E value          3.0e-21
Match length     124
% identity       94
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
                  (ESSA project)

```

```
Seq. No.      163465
Seq. ID       LIB3177-063-P1-K1-D5
Method        BLASTX
NCBI GI       g3834310
BLAST score    644
E value       1.0e-67
Match length  130
% identity    98
NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
come from this gene. [Arabidopsis thaliana]
```

```
Seq. No.      163466
Seq. ID      LIB3177-063-P1-K1-D7
Method       BLASTN
NCBI GI      g2262135
BLAST score   202
E value      1.0e-110
Match length  241
% identity    96
NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                cM, complete sequence
```

```
Seq. No.      163467
Seq. ID      LIB3177-063-P1-K1-D8
Method       BLASTN
NCBI GI      g4741959
BLAST score   34
E value      5.0e-10
Match length  41
% identity    98
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds
```

```
Seq. No.      163468
Seq. ID      LIB3177-063-P1-K1-D9
Method       BLASTX
NCBI GI      g135467
BLAST score   208
E value      4.0e-17
Match length  39
% identity    95
NCBI Description  TUBULIN BETA-4 CHAIN >gi_2129546_pir_S68122 beta-tubulin 4
- Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin
[Arabidopsis thaliana]
```

Seq. No.	163469
Seq. ID	LIB3177-063-P1-K1-E10
Method	BLASTX

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163479
Seq. ID      LIB3177-063-P1-K1-F12
Method       BLASTX
NCBI GI      g548355
BLAST score   459
E value      4.0e-46
Match length  100
% identity    91
NCBI Description  NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate
reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
>gi_22757_emb_CAA79494_(Z19050) nitrate reductase
[Arabidopsis thaliana]>gi_448286_prf__1916406A nitrate
reductase [Arabidopsis thaliana]
```

```
Seq. No.      263480
Seq. ID      LIB3177-063-P1-K1-F2
Method       BLASTX
NCBI GI      g136636
BLAST score   288
E value      9.0e-26
Match length  75
% identity    80
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
                Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin
                Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                [Arabidopsis thaliana]
```

```
Seq. No.      163481
Seq. ID      LIB3177-063-P1-K1-F3
Method       BLASTX
NCBI GI      g1363489
BLAST score   691
E value      4.0e-73
Match length 128
% identity   99
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
glucohydrolase [Arabidopsis thaliana]
```

```
Seq. No.      163482
Seq. ID      LIB3177-063-P1-K1-F4
Method       BLASTX
NCBI GI      g4678260
BLAST score   497
E value      3.0e-50
Match length  121
% identity    86
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]
```

Seq. No. 163483

Seq. ID LIB3177-064-P1-K1-A5
Method BLASTX
NCBI GI g1764100
BLAST score 348
E value 7.0e-33
Match length 67
% identity 99
NCBI Description (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana]

Seq. No. 163509
Seq. ID LIB3177-064-P1-K1-A6
Method BLASTX
NCBI GI g3142289
BLAST score 455
E value 2.0e-45
Match length 94
% identity 90
NCBI Description (AC002411) Strong similarity to beta-keto-CoA synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No. 163510
Seq. ID LIB3177-064-P1-K1-A8
Method BLASTX
NCBI GI g2492952
BLAST score 224
E value 1.0e-18
Match length 95
% identity 88
NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir_S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No. 163511
Seq. ID LIB3177-064-P1-K1-A9
Method BLASTN
NCBI GI g2264307
BLAST score 344
E value 0.0e+00
Match length 445
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 163512
Seq. ID LIB3177-064-P1-K1-B1
Method BLASTX
NCBI GI g1710530
BLAST score 758
E value 6.0e-81
Match length 141
% identity 99
NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir_S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein


```
Method          BLASTX
NCBI GI         g541858
BLAST score     614
E value        8.0e-64
Match length    127
% identity      98
NCBI Description endoxyloglucan transferase - Arabidopsis thaliana
                 >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                 transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                 endo-xyloglucan transferase [Arabidopsis thaliana]
```

```
Seq. No.      163523
Seq. ID      LIB3177-064-P1-K1-C3
Method       BLASTX
NCBI GI      g136636
BLAST score   469
E value      5.0e-47
Match length  87
% identity    99
NCBI Description  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
                Arabidopsis thaliana >gi_442594_pdb_1AAK_Ubiquitin
                Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                [Arabidopsis thaliana]
```

```
Seq. No.      163524
Seq. ID       LIB3177-064-P1-K1-C5
Method        BLASTX
NCBI GI       g2956690
BLAST score   433
E value       6.0e-43
Match length  116
% identity    58
NCBI Description (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928
                 (AF079800) PsbY precursor [Arabidopsis thaliana]
```

Seq. No.	163525
Seq. ID	LIB3177-064-P1-K1-C6
Method	BLASTX
NCBI GI	g2506443
BLAST score	279
E value	4.0e-25
Match length	87
% identity	69
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir_JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]


```
Method          BLASTX
NCBI GI         g2499609
BLAST score     280
E value         3.0e-25
Match length    53
% identity      100
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5)
                 (ATMPK5) >gi_629546_pir_S40471 mitogen-activated protein
                 kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana
                 >gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis
                 thaliana]
```

```
Seq. No.      163537
Seq. ID      LIB3177-064-P1-K1-D7
Method       BLASTX
NCBI GI      g4218120
BLAST score   461
E value      4.0e-46
Match length  116
% identity    78
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis
thaliana]
```

```
Seq. No.      163538
Seq. ID       LIB3177-064-P1-K1-D8
Method        BLASTX
NCBI GI       g3212869
BLAST score   809
E value       7.0e-87
Match length  153
% identity    99
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
```

Seq. No.	163539
Seq. ID	LIB3177-064-P1-K1-D9
Method	BLASTN
NCBI GI	g4584351
BLAST score	284
E value	1.0e-159
Match length	336
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

```
Seq. No.      163540
Seq. ID      LIB3177-064-P1-K1-E10
Method       BLASTX
NCBI GI      g132166
BLAST score   161
E value      3.0e-11
Match length  56
% identity    66
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir_S04048
ribulose-bisphosphate carboxylase activase precursor -
Arabidopsis thaliana >gi_16471_emb_CAA32429 (X14212)
rubisco activase (AA 1 - 473) [Arabidopsis thaliana]
```


BLAST score 173
 E value 2.0e-92
 Match length 392
 % identity 96
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No. 163550
 Seq. ID LIB3177-064-P1-K1-F12
 Method BLASTX
 NCBI GI g2143227
 BLAST score 167
 E value 3.0e-12
 Match length 46
 % identity 74
 NCBI Description (Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No. 163551
 Seq. ID LIB3177-064-P1-K1-F2
 Method BLASTN
 NCBI GI g4468801
 BLAST score 141
 E value 1.0e-73
 Match length 212
 % identity 98
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No. 163552
 Seq. ID LIB3177-064-P1-K1-F4
 Method BLASTX
 NCBI GI g4467099
 BLAST score 389
 E value 5.0e-38
 Match length 75
 % identity 100
 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 163553
 Seq. ID LIB3177-064-P1-K1-F5
 Method BLASTN
 NCBI GI g3449334
 BLAST score 117
 E value 3.0e-59
 Match length 230
 % identity 98
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No. 163554
 Seq. ID LIB3177-064-P1-K1-F7
 Method BLASTX
 NCBI GI g3286693
 BLAST score 632
 E value 3.0e-66
 Match length 127

Seq. ID LIB3177-065-P1-K1-A2
 Method BLASTX
 NCBI GI g3395441
 BLAST score 219
 E value 9.0e-18
 Match length 62
 % identity 58
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 163580
 Seq. ID LIB3177-065-P1-K1-A4
 Method BLASTX
 NCBI GI g1363489
 BLAST score 751
 E value 4.0e-80
 Match length 143
 % identity 95
 NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_(X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 163581
 Seq. ID LIB3177-065-P1-K1-A6
 Method BLASTX
 NCBI GI g2894596
 BLAST score 468
 E value 6.0e-47
 Match length 107
 % identity 85
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 163582
 Seq. ID LIB3177-065-P1-K1-A7
 Method BLASTX
 NCBI GI g2342684
 BLAST score 497
 E value 2.0e-50
 Match length 123
 % identity 84
 NCBI Description (AC000106) F7G19.14 [Arabidopsis thaliana]

Seq. No. 163583
 Seq. ID LIB3177-065-P1-K1-A8
 Method BLASTX
 NCBI GI g135467
 BLAST score 296
 E value 6.0e-27
 Match length 69
 % identity 100
 NCBI Description TUBULIN BETA-4 CHAIN >gi_2129546_pir_S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640_(M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No. 163584
 Seq. ID LIB3177-065-P1-K1-A9
 Method BLASTX
 NCBI GI g1703446

```
BLAST score      194
E value          2.0e-15
Match length     54
% identity       76
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
thaliana]
```

```
Seq. No.      163585
Seq. ID      LIB3177-065-P1-K1-B1
Method       BLASTX
NCBI GI      g115783
BLAST score   557
E value      2.0e-57
Match length  107
% identity    98
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

Seq. No.	163586
Seq. ID	LIB3177-065-P1-K1-B10
Method	BLASTN
NCBI GI	g2737904
BLAST score	67
E value	1.0e-29
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana retrotransposon TSC1 mRNA sequence

Seq. No.	163587
Seq. ID	LIB3177-065-P1-K1-B12
Method	BLASTN
NCBI GI	g2245031
BLAST score	298
E value	1.0e-167
Match length	318
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	163588
Seq. ID	LIB3177-065-P1-K1-B2
Method	BLASTN
NCBI GI	g2191126
BLAST score	318
E value	1.0e-179
Match length	334
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

```
Seq. No.      163589
Seq. ID      LIB3177-065-P1-K1-B3
Method       BLASTX
NCBI GI      q2119848
```



```

NCBI GI      g4220457
BLAST score  493
E value      5.0e-50
Match length 112
% identity   38
NCBI Description (AC006216) Similar to gi_3413714 T19L18.21 putative
myrosinase-binding protein from Arabidopsis thaliana BAC
gb_AC004747. EST gb_N96478 comes from this gene.
[Arabidopsis thaliana]

```

```
Seq. No.      163594
Seq. ID      LIB3177-065-P1-K1-C1
Method       BLASTX
NCBI GI      g140508
BLAST score   308
E value      8.0e-29
Match length  65
% identity    88
NCBI Description  PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable
maturase, 63K - white mustard chloroplast
>gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis
alba]
```

Seq. No.	163595
Seq. ID	LIB3177-065-P1-K1-C10
Method	BLASTN
NCBI GI	g4741961
BLAST score	216
E value	1.0e-118
Match length	238
% identity	98
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

```
Seq. No.      163596
Seq. ID      LIB3177-065-P1-K1-C11
Method       BLASTX
NCBI GI      g1488255
BLAST score   346
E value      1.0e-32
Match length  90
% identity    69
NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
>gi_2961381_emb_CAA18128_(AL022141) ferulate-5-hydroxylase
[FAH1] [Arabidopsis thaliana] >gi_3925365 (AF068574)
ferulate-5-hydroxylase [Arabidopsis thaliana]
```

```
Seq. No.      163597
Seq. ID       LIB3177-065-P1-K1-C12
Method        BLASTN
NCBI GI       g4662609
BLAST score    76
E value       5.0e-35
Match length   159
% identity     91
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,
                complete sequence
```

Seq. No. 163598
 Seq. ID LIB3177-065-P1-K1-C2
 Method BLASTX
 NCBI GI g3286693
 BLAST score 573
 E value 2.0e-59
 Match length 118
 % identity 99
 NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No. 163599
 Seq. ID LIB3177-065-P1-K1-C3
 Method BLASTX
 NCBI GI g115767
 BLAST score 589
 E value 3.0e-61
 Match length 116
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
 >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]
 >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163600
 Seq. ID LIB3177-065-P1-K1-C7
 Method BLASTN
 NCBI GI g2760165
 BLAST score 209
 E value 1.0e-114
 Match length 275
 % identity 99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 163601
 Seq. ID LIB3177-065-P1-K1-C8
 Method BLASTX
 NCBI GI g131211
 BLAST score 176
 E value 4.0e-13
 Match length 36
 % identity 94
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J)
 >gi_1363533_pir_S58571 photosystem I protein psaJ - maize chloroplast >gi_552734 (J04502) ORF42 [Zea mays]
 >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]

Seq. No. 163602
 Seq. ID LIB3177-065-P1-K1-C9
 Method BLASTX
 NCBI GI g1514639
 BLAST score 86
 E value 3.0e-17

Match length	62
% identity	77
NCBI Description	(X85181) alpha-glucan phosphorylase [<i>Spinacia oleracea</i>]
Seq. No.	163603
Seq. ID	LIB3177-065-P1-K1-D1
Method	BLASTX
NCBI GI	g3355472
BLAST score	152
E value	2.0e-10
Match length	41
% identity	66
NCBI Description	(AC004218) disease resistance response protein (206-d) like [<i>Arabidopsis thaliana</i>]
Seq. No.	163604
Seq. ID	LIB3177-065-P1-K1-D10
Method	BLASTX
NCBI GI	g4220514
BLAST score	83
E value	4.0e-09
Match length	54
% identity	61
NCBI Description	(AL035356) putative protein [<i>Arabidopsis thaliana</i>]
Seq. No.	163605
Seq. ID	LIB3177-065-P1-K1-D11
Method	BLASTX
NCBI GI	g3236248
BLAST score	304
E value	6.0e-28
Match length	88
% identity	70
NCBI Description	(AC004684) unknown protein [<i>Arabidopsis thaliana</i>]
Seq. No.	163606
Seq. ID	LIB3177-065-P1-K1-D2
Method	BLASTX
NCBI GI	g1703220
BLAST score	441
E value	1.0e-43
Match length	141
% identity	57
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [<i>Arabidopsis thaliana</i>]
Seq. No.	163607
Seq. ID	LIB3177-065-P1-K1-D4
Method	BLASTX
NCBI GI	g227070
BLAST score	165
E value	1.0e-11
Match length	42
% identity	71
NCBI Description	ribosomal protein CS-S5 [<i>Spinacia oleracea</i>]
Seq. No.	163608

Seq. No.	163623
Seq. ID	LIB3177-065-P1-K1-F1
Method	BLASTN
NCBI GI	g3687221
BLAST score	58
E value	2.0e-24
Match length	86
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163624
Seq. ID	LIB3177-065-P1-K1-F10
Method	BLASTN
NCBI GI	g4589444
BLAST score	58
E value	3.0e-24
Match length	140
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence
Seq. No.	163625
Seq. ID	LIB3177-065-P1-K1-F4
Method	BLASTX
NCBI GI	g4006879
BLAST score	581
E value	2.0e-60
Match length	113
% identity	100
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.	163626
Seq. ID	LIB3177-065-P1-K1-F5
Method	BLASTX
NCBI GI	g3953473
BLAST score	452
E value	4.0e-45
Match length	117
% identity	80
NCBI Description	(AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.	163627
Seq. ID	LIB3177-065-P1-K1-F7
Method	BLASTN
NCBI GI	g4589428
BLAST score	265
E value	1.0e-147
Match length	289
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence
Seq. No.	163628
Seq. ID	LIB3177-065-P1-K1-F8
Method	BLASTX
NCBI GI	g4567235

Seq. ID	LIB3177-065-P1-K1-H12
Method	BLASTX
NCBI GI	g2244881
BLAST score	512
E value	4.0e-52
Match length	103
% identity	61
NCBI Description	(Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]

```
Seq. No.      163644
Seq. ID      LIB3177-065-P1-K1-H3
Method       BLASTX
NCBI GI      g2559012
BLAST score   361
E value      1.0e-34
Match length  92
% identity    76
NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1,
beta subunit; CCT-beta [Homo sapiens] >gi_4090929
(AF026166) chaperonin-containing TCP-1 beta subunit homolog
[Homo sapiens]
```

```
Seq. No.      163645
Seq. ID      LIB3177-065-P1-K1-H4
Method       BLASTX
NCBI GI      g115783
BLAST score   618
E value      2.0e-64
Match length  116
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

Seq. No.	163646
Seq. ID	LIB3177-065-P1-K1-H6
Method	BLASTX
NCBI GI	g3892714
BLAST score	611
E value	1.0e-63
Match length	130
% identity	94
NCBI Description	(AL033545) trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	163647
Seq. ID	LIB3177-065-P1-K1-H7
Method	BLASTN
NCBI GI	g1769904
BLAST score	120
E value	3.0e-61
Match length	144
% identity	97
NCBI Description	A.thaliana psbP gene

Seq. No. 163648

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence
Seq. No.	163658
Seq. ID	LIB3177-066-P1-K1-B12
Method	BLASTX
NCBI GI	g2062161
BLAST score	463
E value	3.0e-47
Match length	102
% identity	52
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	163659
Seq. ID	LIB3177-066-P1-K1-B2
Method	BLASTN
NCBI GI	g2182287
BLAST score	73
E value	4.0e-33
Match length	129
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	163660
Seq. ID	LIB3177-066-P1-K1-B3
Method	BLASTN
NCBI GI	g2980757
BLAST score	140
E value	3.0e-73
Match length	152
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

```
Seq. No.      163661
Seq. ID      LIB3177-066-P1-K1-B6
Method       BLASTX
NCBI GI      g1402878
BLAST score   263
E value      3.0e-23
Match length  93
% identity    58
NCBI Description (X98130) unknown [Arabidopsis thaliana]
```

Seq. No.	163662
Seq. ID	LIB3177-066-P1-K1-B8
Method	BLASTX
NCBI GI	g1619300
BLAST score	182
E value	8.0e-14
Match length	51
% identity	71
NCBI Description	(X95269) LRR protein [<i>Lycopersicon esculentum</i>]

Seq. No.	163663
Seq. ID	LIB3177-066-P1-K1-C12
Method	BLASTN
NCBI GI	g2335089
BLAST score	102
E value	3.0e-50
Match length	126
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163664
Seq. ID	LIB3177-066-P1-K1-C2
Method	BLASTN
NCBI GI	g16473
BLAST score	375
E value	0.0e+00
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

```
Seq. No.      163665
Seq. ID      LIB3177-066-P1-K1-C4
Method       BLASTX
NCBI GI      g2499535
BLAST score   352
E value      9.0e-34
Match length  82
% identity    80
NCBI Description  2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
                (U13238) 2-oxoglutarate/malate translocator [Spinacia
                oleracea]
```

```
Seq. No.      163666
Seq. ID      LIB3177-066-P1-K1-C5
Method       BLASTN
NCBI GI      g2264316
BLAST score   86
E value      2.0e-40
Match length  427
% identity    39
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                MRO11, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.      163667
Seq. ID       LIB3177-066-P1-K1-C7
Method        BLASTN
NCBI GI       g3540210
BLAST score   41
E value       2.0e-14
Match length  77
% identity    90
NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic
sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No.	163668
Seq. ID	LIB3177-066-P1-K1-C8

[illegible]


```
BLAST score      348
E value         8.0e-33
Match length    71
% identity      48
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
```

```
Seq. No.      163674
Seq. ID      LIB3177-066-P1-K1-D4
Method       BLASTX
NCBI GI      g2497733
BLAST score   203
E value      2.0e-16
Match length  53
% identity    65
NCBI Description  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                >gi_1177796 (M80567) non-specific lipid transfer protein
                [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
                protein [Arabidopsis thaliana]
```

```
Seq. No.      163675
Seq. ID      LIB3177-066-P1-K1-D5
Method       BLASTX
NCBI GI      g841208
BLAST score   309
E value      3.0e-28
Match length  128
% identity    55
NCBI Description (U18995) trypsin inhibitor propeptide [Brassica oleracea]
```

Seq. No.	163676
Seq. ID	LIB3177-066-P1-K1-D7
Method	BLASTN
NCBI GI	g2642427
BLAST score	58
E value	8.0e-24
Match length	94
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163677
Seq. ID	LIB3177-066-P1-K1-D8
Method	BLASTN
NCBI GI	g17681
BLAST score	52
E value	3.0e-20
Match length	208
% identity	88
NCBI Description	A.thaliana mRNA for Wilm's tumor suppressor homologue

```
Seq. No.      163678
Seq. ID       LIB3177-066-P1-K1-D9
Method        BLASTX
NCBI GI       g4510373
BLAST score   323
E value       7.0e-30
```


Seq. No.	163683
Seq. ID	LIB3177-066-P1-K1-E3
Method	BLASTX
NCBI GI	g2791423
BLAST score	192
E value	1.0e-14
Match length	69
% identity	54
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

```
Seq. No.          163684
Seq. ID           LIB3177-066-P1-K1-E4
Method            BLASTX
NCBI GI           g2129636
BLAST score       724
E value           6.0e-77
Match length      153
% identity        91
NCBI Description   lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
                  [Arabidopsis thaliana]
```

```
Seq. No.      163685
Seq. ID      LIB3177-066-P1-K1-E5
Method       BLASTX
NCBI GI      g2129636
BLAST score   278
E value      1.0e-24
Match length  86
% identity    65
NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
               [Arabidopsis thaliana]
```

```
Seq. No.      163686
Seq. ID      LIB3177-066-P1-K1-E6
Method       BLASTX
NCBI GI      g2462077
BLAST score   397
E value      7.0e-39
Match length  82
% identity    95
NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]
```

```
Seq. No.      163687
Seq. ID      LIB3177-066-P1-K1-E8
Method       BLASTX
NCBI GI      g2791423
BLAST score   207
E value      3.0e-16
Match length  71
% identity    55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
```

```
Seq. No.      163688
Seq. ID       LIB3177-066-P1-K1-E9
Method        BLASTX
NCBI GI       q2462825
```


>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 163703
Seq. ID LIB3177-066-P1-K1-G6
Method BLASTN
NCBI GI g1167960
BLAST score 42
E value 3.0e-14
Match length 244
% identity 30
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds

Seq. No. 163704
Seq. ID LIB3177-066-P1-K1-G7
Method BLASTX
NCBI GI g2244798
BLAST score 324
E value 4.0e-30
Match length 62
% identity 100
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163705
Seq. ID LIB3177-066-P1-K1-G8
Method BLASTX
NCBI GI g1769905
BLAST score 455
E value 2.0e-45
Match length 129
% identity 69
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving complex (OEC) [Arabidopsis thaliana]

Seq. No. 163706
Seq. ID LIB3177-066-P1-K1-G9
Method BLASTX
NCBI GI g4741960
BLAST score 155
E value 1.0e-46
Match length 139
% identity 74
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 163707
Seq. ID LIB3177-066-P1-K1-H10
Method BLASTN
NCBI GI g3413696
BLAST score 297
E value 1.0e-166
Match length 305
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163708
Seq. ID	LIB3177-066-P1-K1-H2
Method	BLASTX
NCBI GI	g282865
BLAST score	323
E value	3.0e-30
Match length	71
% identity	85
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	163709
Seq. ID	LIB3177-066-P1-K1-H3
Method	BLASTX
NCBI GI	g1170373
BLAST score	668
E value	3.0e-70
Match length	130
% identity	98
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	163710
Seq. ID	LIB3177-066-P1-K1-H4
Method	BLASTN
NCBI GI	g2062153
BLAST score	102
E value	3.0e-50
Match length	110
% identity	98
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163711
Seq. ID	LIB3177-066-P1-K1-H5
Method	BLASTN
NCBI GI	g4006885
BLAST score	58
E value	3.0e-24
Match length	58
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	163712
Seq. ID	LIB3177-066-P1-K1-H6
Method	BLASTN
NCBI GI	g469113
BLAST score	345
E value	0.0e+00

Match length	357
% identity	99
NCBI Description	A.thaliana (Columbia) Dr4 mRNA
Seq. No.	163713
Seq. ID	LIB3177-066-P1-K1-H7
Method	BLASTX
NCBI GI	g4510402
BLAST score	80
E value	1.2e-01
Match length	109
% identity	45
NCBI Description	(AC006587) putative AP2 domain [Arabidopsis thaliana]
Seq. No.	163714
Seq. ID	LIB3177-066-P1-K1-H8
Method	BLASTX
NCBI GI	g1702987
BLAST score	529
E value	4.0e-54
Match length	107
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]
Seq. No.	163715
Seq. ID	LIB3177-066-P1-K1-H9
Method	BLASTN
NCBI GI	g4559375
BLAST score	151
E value	2.0e-79
Match length	245
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence
Seq. No.	163716
Seq. ID	LIB3177-067-P1-K1-A10
Method	BLASTN
NCBI GI	g469113
BLAST score	393
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	A.thaliana (Columbia) Dr4 mRNA
Seq. No.	163717
Seq. ID	LIB3177-067-P1-K1-A12
Method	BLASTX
NCBI GI	g2832683
BLAST score	332
E value	6.0e-31
Match length	65
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. ID	LIB3177-067-P1-K1-A8
Method	BLASTX
NCBI GI	g2493810
BLAST score	237
E value	4.0e-20
Match length	43
% identity	98
NCBI Description	COPROPORPHYRINOGEN III OXIDASE PRECURSOR (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) >gi_1213067_emb_CAA58038_ (X82831) coproporphyrinogen oxidase [Nicotiana tabacum]
Seq. No.	163724
Seq. ID	LIB3177-067-P1-K1-B1
Method	BLASTX
NCBI GI	g3287862
BLAST score	339
E value	5.0e-32
Match length	63
% identity	95
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]
Seq. No.	163725
Seq. ID	LIB3177-067-P1-K1-B10
Method	BLASTN
NCBI GI	g4580744
BLAST score	133
E value	4.0e-69
Match length	137
% identity	56
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence
Seq. No.	163726
Seq. ID	LIB3177-067-P1-K1-B11
Method	BLASTX
NCBI GI	g549010
BLAST score	701
E value	3.0e-74
Match length	137
% identity	100
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir_S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]
Seq. No.	163727
Seq. ID	LIB3177-067-P1-K1-B12
Method	BLASTN

NCBI GI	g4406805
BLAST score	281
E value	1.0e-157
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163728
Seq. ID	LIB3177-067-P1-K1-B2
Method	BLASTN
NCBI GI	g4199934
BLAST score	91
E value	4.0e-44
Match length	103
% identity	74
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]
Seq. No.	163729
Seq. ID	LIB3177-067-P1-K1-B4
Method	BLASTX
NCBI GI	g132110
BLAST score	356
E value	4.0e-34
Match length	76
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	163730
Seq. ID	LIB3177-067-P1-K1-B5
Method	BLASTN
NCBI GI	g4544381
BLAST score	75
E value	5.0e-34
Match length	79
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence
Seq. No.	163731
Seq. ID	LIB3177-067-P1-K1-B6
Method	BLASTX
NCBI GI	g4337175
BLAST score	520
E value	5.0e-53
Match length	131
% identity	79
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	163737
Seq. ID	LIB3177-067-P1-K1-C2
Method	BLASTX
NCBI GI	g3355480
BLAST score	242
E value	2.0e-20
Match length	79
% identity	56
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

```
Seq. No.      163738
Seq. ID      LIB3177-067-P1-K1-C3
Method       BLASTN
NCBI GI      g2618720
BLAST score   132
E value      3.0e-68
Match length  172
% identity    95
NCBI Description Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
                complete cds
```

```
Seq. No.      163739
Seq. ID      LIB3177-067-P1-K1-C5
Method       BLASTX
NCBI GI      g4056503
BLAST score   169
E value      3.0e-12
Match length  36
% identity    92
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      163740
Seq. ID       LIB3177-067-P1-K1-C7
Method        BLASTX
NCBI GI       g1621268
BLAST score    373
E value       5.0e-36
Match length   107
% identity     68
NCBI Description (Z81012) unknown [Ricinus communis]
```

```
Seq. No.      163741
Seq. ID      LIB3177-067-P1-K1-C8
Method       BLASTX
NCBI GI      g113026
BLAST score   614
E value      5.0e-64
Match length  132
% identity    89
NCBI Description  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
>gi_68211_pir_WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
isocitrate lyase [Brassica napus] >gi_447142 prf_1913424A
```


Seq. ID	LIB3177-067-P1-K1-D5
Method	BLASTN
NCBI GI	g4309683
BLAST score	98
E value	4.0e-48
Match length	154
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	163748
Seq. ID	LIB3177-067-P1-K1-D6
Method	BLASTN
NCBI GI	g3883125
BLAST score	297
E value	1.0e-166
Match length	388
% identity	95
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, complete cds
Seq. No.	163749
Seq. ID	LIB3177-067-P1-K1-D8
Method	BLASTN
NCBI GI	g3929648
BLAST score	177
E value	4.0e-95
Match length	205
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for mitochondrial NAD-dependent malate dehydrogenase
Seq. No.	163750
Seq. ID	LIB3177-067-P1-K1-E1
Method	BLASTN
NCBI GI	g3299824
BLAST score	43
E value	7.0e-16
Match length	61
% identity	92
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	163751
Seq. ID	LIB3177-067-P1-K1-E10
Method	BLASTN
NCBI GI	g16470
BLAST score	98
E value	3.0e-48
Match length	118
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for rubisco activase
Seq. No.	163752
Seq. ID	LIB3177-067-P1-K1-E12
Method	BLASTN
NCBI GI	g950098

```
BLAST score      163
E value         8.0e-87
Match length    187
% identity      97
NCBI Description Arabidopsis thaliana gibberellin-regulated (GASA4) mRNA,
                  complete cds
```

```
Seq. No.      163753
Seq. ID      LIB3177-067-P1-K1-E2
Method       BLASTX
NCBI GI      g115767
BLAST score   650
E value      3.0e-68
Match length 127
% identity    98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll
a/b-binding protein ab165 - Arabidopsis thaliana
>gi_16368_emb_CAA27540_(X03907) chlorophyll a/b binding
protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_(X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]
```

Seq. No.	163754
Seq. ID	LIB3177-067-P1-K1-E5
Method	BLASTN
NCBI GI	g47594
BLAST score	85
E value	4.0e-40
Match length	161
% identity	91
NCBI Description	Synechocystis sp. ndhE gene (partial), psaC gene for photosystem I iron-sulfur protein and ndhD-like ORF

```
Seq. No.      163755
Seq. ID      LIB3177-067-P1-K1-E6
Method       BLASTN
NCBI GI      g3283056
BLAST score   48
E value      3.0e-18
Match length  127
% identity    84
NCBI Description Arabidopsis thaliana one helix protein (OHP) mRNA, complete cds
```

```
Seq. No.      163756
Seq. ID      LIB3177-067-P1-K1-E7
Method       BLASTX
NCBI GI      g132110
BLAST score   393
E value      2.0e-38
Match length  79
% identity    96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
```


BLAST score 365
 E value 6.0e-35
 Match length 118
 % identity 64
 NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
 (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir_S52286 NADH
 dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
 >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase
 [Arabidopsis thaliana]

Seq. No. 163762
 Seq. ID LIB3177-067-P1-K1-F3
 Method BLASTX
 NCBI GI g4454479
 BLAST score 356
 E value 7.0e-34
 Match length 74
 % identity 97
 NCBI Description (AC006234) putative riboflavin synthase alpha chain
 [Arabidopsis thaliana]

Seq. No. 163763
 Seq. ID LIB3177-067-P1-K1-F4
 Method BLASTX
 NCBI GI g1175013
 BLAST score 221
 E value 1.0e-18
 Match length 42
 % identity 98
 NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir_S44084
 plasma membrane intrinsic protein 2a - Arabidopsis thaliana
 >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
 protein 2a [Arabidopsis thaliana]

Seq. No. 163764
 Seq. ID LIB3177-067-P1-K1-F9
 Method BLASTX
 NCBI GI g3157937
 BLAST score 259
 E value 1.0e-22
 Match length 60
 % identity 82
 NCBI Description (AC002131) Identical to aspartic proteinase cDNA gb_U51036
 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
 gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
 gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
 gb_AA728734, gb

Seq. No. 163765
 Seq. ID LIB3177-067-P1-K1-G1
 Method BLASTX
 NCBI GI g2493052
 BLAST score 373
 E value 5.0e-36
 Match length 70
 % identity 100
 NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL

```
>gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of  
mitochondrial F1-ATPase [Arabidopsis thaliana]
```

```
Seq. No.      163766
Seq. ID      LIB3177-067-P1-K1-G11
Method       BLASTX
NCBI GI      g4538903
BLAST score   139
E value      9.0e-09
Match length  72
% identity    43
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163767
Seq. ID      LIB3177-067-P1-K1-G12
Method       BLASTX
NCBI GI      g3695383
BLAST score   250
E value      1.0e-21
Match length  61
% identity    82
NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:
PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
thaliana]
```

Seq. No.	163768
Seq. ID	LIB3177-067-P1-K1-G2
Method	BLASTX
NCBI GI	g2911042
BLAST score	357
E value	2.0e-34
Match length	72
% identity	100
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	163769
Seq. ID	LIB3177-067-P1-K1-G3
Method	BLASTX
NCBI GI	g4490732
BLAST score	567
E value	1.0e-58
Match length	120
% identity	88
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

```
Seq. No.      163770
Seq. ID      LIB3177-067-P1-K1-G4
Method       BLASTX
NCBI GI      g2815905
BLAST score   290
E value      4.0e-26
Match length  98
% identity    58
NCBI Description (AF043734) Pros45 proteosome subunit homolog [Drosophila
melanogaster]
```



```

BLAST score      624
E value          2.0e-66
Match length     132
% identity       98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603_pir_A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]

```

```
Seq. No.      163776
Seq. ID       LIB3177-067-P1-K1-H11
Method        BLASTX
NCBI GI       g1732570
BLAST score    277
E value       3.0e-25
Match length   73
% identity     77
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
```

```
Seq. No.      163777
Seq. ID      LIB3177-067-P1-K1-H12
Method       BLASTX
NCBI GI      g115385
BLAST score   687
E value      1.0e-72
Match length  131
% identity    100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
chlorophyll a/b binding protein [Arabidopsis thaliana]
```

Seq. No.	163778
Seq. ID	LIB3177-067-P1-K1-H2
Method	BLASTN
NCBI GI	g3212846
BLAST score	200
E value	1.0e-109
Match length	244
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	163779
Seq. ID	LIB3177-067-P1-K1-H3
Method	BLASTN
NCBI GI	g4056476
BLAST score	113
E value	7.0e-57
Match length	194
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163780

Figure 1 displays 15 bar charts showing the percentage of respondents for various demographic and attitudinal variables. The variables are listed on the left, and the percentage ranges are shown on the right. The charts are arranged in a grid-like fashion, with some variables having multiple bars representing different categories.

Variable	Percentage Range
Age	18-24, 25-34, 35-44, 45-54, 55-64, 65+
Gender	Male, Female
Ethnicity	White, Black, Hispanic, Asian, Other
Education	High School, Some College, Bachelor's, Master's, Doctorate
Income	\$0-\$10,000, \$10,000-\$20,000, \$20,000-\$30,000, \$30,000-\$40,000, \$40,000-\$50,000, \$50,000-\$60,000, \$60,000-\$70,000, \$70,000-\$80,000, \$80,000-\$90,000, \$90,000-\$100,000, \$100,000+
Marital Status	Single, Married, Divorced, Widowed
Religion	Protestant, Catholic, Jewish, Muslim, Other
Political Affiliation	Democrat, Republican, Independent
Attitude Toward the Environment	Very Concerned, Concerned, Not Concerned
Attitude Toward Global Warming	Very Concerned, Concerned, Not Concerned
Attitude Toward Climate Change	Very Concerned, Concerned, Not Concerned
Attitude Toward Air Pollution	Very Concerned, Concerned, Not Concerned
Attitude Toward Water Pollution	Very Concerned, Concerned, Not Concerned
Attitude Toward Land Use	Very Concerned, Concerned, Not Concerned
Attitude Toward Deforestation	Very Concerned, Concerned, Not Concerned
Attitude Toward Biodiversity	Very Concerned, Concerned, Not Concerned

BLAST score 561
 E value 8.0e-58
 Match length 109
 % identity 98
 NCBI Description (AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No. 163785
 Seq. ID LIB3177-068-P1-K1-A11
 Method BLASTX
 NCBI GI g118514
 BLAST score 179
 E value 2.0e-25
 Match length 88
 % identity 65
 NCBI Description TURGOR-RESPONSIVE PROTEIN 26G >gi_100051_pir_S11863 aldehyde dehydrogenase homolog - garden pea >gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum sativum]

Seq. No. 163786
 Seq. ID LIB3177-068-P1-K1-A12
 Method BLASTN
 NCBI GI g3421079
 BLAST score 353
 E value 0.0e+00
 Match length 357
 % identity 100
 NCBI Description Arabidopsis thaliana 20S proteasome subunit PAD1 (PAD1) mRNA, complete cds

Seq. No. 163787
 Seq. ID LIB3177-068-P1-K1-A2
 Method BLASTX
 NCBI GI g132110
 BLAST score 582
 E value 2.0e-60
 Match length 116
 % identity 96
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 163788
 Seq. ID LIB3177-068-P1-K1-A3
 Method BLASTN
 NCBI GI g2244829
 BLAST score 228
 E value 1.0e-125
 Match length 404
 % identity 98


```
Seq. No.          163794
Seq. ID           LIB3177-068-P1-K1-B10
Method            BLASTX
NCBI GI           g131398
BLAST score       554
E value           5.0e-57
Match length      140
% identity        81
NCBI Description  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir_F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
```

Seq. No.	163795
Seq. ID	LIB3177-068-P1-K1-B11
Method	BLASTX
NCBI GI	g2062161
BLAST score	588
E value	4.0e-61
Match length	128
% identity	53
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	163796
Seq. ID	LIB3177-068-P1-K1-B12
Method	BLASTN
NCBI GI	g438448
BLAST score	34
E value	4.0e-10
Match length	38
% identity	97
NCBI Description	Arabidopsis thaliana carbonic anhydrase (ca180) mRNA, complete cds

Seq. No.	163797
Seq. ID	LIB3177-068-P1-K1-B2
Method	BLASTX
NCBI GI	g4741940
BLAST score	536
E value	6.0e-55
Match length	118
% identity	60
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

```
Seq. No.      163798
Seq. ID      LIB3177-068-P1-K1-B3
Method       BLASTN
NCBI GI      g2760169
BLAST score   186
E value      1.0e-100
```



```
Seq. ID      LIB3177-068-P1-K1-D2
Method       BLASTX
NCBI GI      g132074
BLAST score   517
E value      7.0e-53
Match length 105
% identity    95
NCBI Description  RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir_RKMUA1
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                A1 precursor - Arabidopsis thaliana
```

```
Seq. No.      163819
Seq. ID       LIB3177-068-P1-K1-D3
Method        BLASTN
NCBI GI       g2459406
BLAST score    202
E value        1.0e-110
Match length   402
% identity     99
NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic
sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No.	163820
Seq. ID	LIB3177-068-P1-K1-D4
Method	BLASTN
NCBI GI	g4519194
BLAST score	257
E value	1.0e-142
Match length	288
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

```
Seq. No.      163821
Seq. ID      LIB3177-068-P1-K1-D5
Method       BLASTX
NCBI GI      g1370186
BLAST score   516
E value      2.0e-52
Match length  101
% identity    98
NCBI Description (Z73942) RAB7C [Lotus japonicus]
```

```
Seq. No.      163822
Seq. ID      LIB3177-068-P1-K1-D6
Method       BLASTX
NCBI GI      g4582787
BLAST score   334
E value      2.0e-31
Match length  77
% identity    83
NCBI Description (AJ012281) adenosine kinase [Zea mays]
```

Seq. No.	163823
Seq. ID	LIB3177-068-P1-K1-D7
Method	BLASTX

Seq. No.	163833
Seq. ID	LIB3177-068-P1-K1-E5
Method	BLASTX
NCBI GI	g4586256
BLAST score	247
E value	4.0e-21
Match length	62
% identity	81
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	163834
Seq. ID	LIB3177-068-P1-K1-E6
Method	BLASTN
NCBI GI	g3869069
BLAST score	56
E value	1.0e-22
Match length	389
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163835
Seq. ID      LIB3177-068-P1-K1-E7
Method       BLASTX
NCBI GI      g115783
BLAST score   508
E value      9.0e-52
Match length  95
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
```

```
Seq. No.      163836
Seq. ID      LIB3177-068-P1-K1-F1
Method       BLASTX
NCBI GI      g421826
BLAST score   618
E value      2.0e-64
Match length  141
% identity    82
NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                thaliana]
```

Seq. No.	163837
Seq. ID	LIB3177-068-P1-K1-F10
Method	BLASTX
NCBI GI	g4741960
BLAST score	478
E value	4.0e-48
Match length	111
% identity	82
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]


```
Seq. No.      163848
Seq. ID      LIB3177-068-F1-K1-G12
Method       BLASTX
NCBI GI      g4539009
BLAST score   661
E value      2.0e-69
Match length  156
% identity    76
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      163849
Seq. ID      LIB3177-068-P1-K1-G2
Method       BLASTX
NCBI GI      g1175010
BLAST score   317
E value      1.0e-46
Match length 113
% identity   88
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir_S44082
                plasma membrane intrinsic protein 1a - Arabidopsis thaliana
                >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                protein 1a [Arabidopsis thaliana]
```

[illegible]

Seq. No.	163851
Seq. ID	LIB3177-068-P1-K1-G5
Method	BLASTN
NCBI GI	g4589412
BLAST score	46
E value	1.0e-16
Match length	155
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

```
Seq. No.      163852
Seq. ID       LIB3177-068-P1-K1-G6
Method        BLASTX
NCBI GI       g3914442
BLAST score    424
E value       7.0e-42
```

Variable	Mean	SD	Min	Max
1. age (years)	37.5	10.5	18	65
2. sex (male = 1, female = 2)	1.5	0.7	1	2
3. education (years)	12.5	2.5	8	16
4. income (€)	1500	500	500	3000
5. employment (yes = 1, no = 2)	1.2	0.4	1	2
6. health status (good = 1, bad = 2)	1.3	0.5	1	2
7. family size (persons)	2.5	1.0	1	5
8. housing (own = 1, rent = 2)	1.4	0.5	1	2
9. car ownership (yes = 1, no = 2)	1.1	0.3	1	2
10. internet usage (yes = 1, no = 2)	1.2	0.4	1	2
11. smoking (yes = 1, no = 2)	1.3	0.5	1	2
12. alcohol consumption (yes = 1, no = 2)	1.4	0.5	1	2
13. exercise frequency (times/week)	2.0	1.5	0	5
14. diet quality (score)	75	10	50	100
15. stress level (low = 1, medium = 2, high = 3)	1.8	0.8	1	3
16. sleep quality (good = 1, poor = 2)	1.3	0.5	1	2
17. social support (yes = 1, no = 2)	1.2	0.4	1	2
18. life satisfaction (score)	70	15	50	100
19. mental health (yes = 1, no = 2)	1.1	0.3	1	2
20. physical health (yes = 1, no = 2)	1.2	0.4	1	2

NCBI Description (AC006532) putative zinc-finger protein [Arabidopsis thaliana]

```
Seq. No.      163858
Seq. ID      LIB3177-068-P1-K1-H12
Method       BLASTX
NCBI GI      g2894564
BLAST score   127
E value      9.0e-28
Match length  66
% identity   98
NCBI Description (AL021890) putative p
```

Seq. No.	163859
Seq. ID	LIB3177-068-P1-K1-H2
Method	BLASTN
NCBI GI	g3298610
BLAST score	127
E value	2.0e-65
Match length	135
% identity	99
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	163860
Seq. ID	LIB3177-068-P1-K1-H3
Method	BLASTN
NCBI GI	g2760829
BLAST score	297
E value	1.0e-166
Match length	324
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.      163861
Seq. ID      LIB3177-068-P1-K1-H4
Method       BLASTX
NCBI GI      g2146741
BLAST score   630
E value      5.0e-66
Match length  119
% identity    100
NCBI Description isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl
diphosphate:dimethylallyl diphosphate isomerase
[Arabidopsis thaliana]
```

```
Seq. No.      163862
Seq. ID      LIB3177-068-P1-K1-H5
Method       BLASTX
NCBI GI      g1477480
BLAST score   739
E value      1.0e-78
Match length  145
% identity    52
NCBI Description (U40341) carbamoyl phosphate synthetase large chain
               [Arabidopsis thaliana]
```



```
Seq. No.      163863
Seq. ID      LIB3177-068-P1-K1-H6
Method       BLASTX
NCBI GI      g3449041
BLAST score   486
E value      3.0e-49
Match length  90
% identity    97
NCBI Description (U73462) carbonic anhydrase [Arabidopsis thaliana]
```

Seq. No.	163864
Seq. ID	LIB3177-068-P1-K1-H7
Method	BLASTN
NCBI GI	g4159706
BLAST score	104
E value	7.0e-52
Match length	127
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

```
Seq. No.      163865
Seq. ID      LIB3177-068-P1-K1-H8
Method       BLASTX
NCBI GI      g166835
BLAST score   525
E value      7.0e-54
Match length  100
% identity    100
NCBI Description (M86720) ribulose biphosphate carboxylase/oxygenase
activase [Arabidopsis thaliana] >gi_2642170 (AC003000)
Rubisco activase [Arabidopsis thaliana]
```

Seq. No.	163866
Seq. ID	LIB3177-068-P1-K1-H9
Method	BLASTN
NCBI GI	g600388
BLAST score	285
E value	1.0e-159
Match length	306
% identity	98
NCBI Description	A.thaliana UbcAT3 mRNA for ubiquitin conjugating enzyme E2

```
Seq. No.          163867
Seq. ID           LIB3177-069-P1-K1-A10
Method            BLASTN
NCBI GI           g4519192
BLAST score       258
E value           1.0e-143
Match length      262
% identity        100
NCBI Description   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
```

Seq. No.	163868
Seq. ID	LIB3177-069-P1-K1-A11

Figure 1 consists of 15 histograms arranged vertically, each representing a different value of n from 1 to 15. The x-axis for all histograms is 'Number of non-zero elements in z ' with major ticks at 0, 5, 10, and 15. The y-axis is 'Frequency' with major ticks at 0, 5, and 10. The histograms show a unimodal distribution that shifts to the right as n increases. For $n=1$, the peak is at 1. For $n=15$, the peak is at 15.

Match length	95
% identity	89
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

```
Seq. No.          163923
Seq. ID           LIB3177-069-P1-K1-H11
Method            BLASTX
NCBI GI           g3914117
BLAST score       582
E value           3.0e-60
Match length      144
% identity        81
NCBI Description  NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP
                  KINASE II) >gi_3093480 (AF017640) nucleoside diphosphate
                  kinase type 2 [Arabidopsis thaliana]
```

```
Seq. No.      163924
Seq. ID      LIB3177-069-P1-K1-H12
Method       BLASTX
NCBI GI      g4566505
BLAST score   262
E value      4.0e-23
Match length  84
% identity    60
NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
               [Hordeum vulgare]
```

```
Seq. No.      163925
Seq. ID      LIB3177-069-P1-K1-H2
Method       BLASTX
NCBI GI      g3080401
BLAST score   587
E value      7.0e-61
Match length  116
% identity    100
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
               >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
               [Arabidopsis thaliana]
```

```
Seq. No.      163926
Seq. ID      LIB3177-069-P1-K1-H3
Method       BLASTN
NCBI GI      g3402745
BLAST score   166
E value      3.0e-88
Match length  268
% identity    93
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                (ESSAII project)
```

Seq. No.	163927
Seq. ID	LIB3177-069-P1-K1-H4
Method	BLASTN
NCBI GI	q4519185

Seq. No.	163994
Seq. ID	LIB3177-070-P1-K1-G2
Method	BLASTN
NCBI GI	g4756963
BLAST score	231
E value	1.0e-127
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

```
Seq. No.      163995
Seq. ID      LIB3177-070-P1-K1-G3
Method       BLASTX
NCBI GI      g1351271
BLAST score   185
E value      9.0e-14
Match length  41
% identity    90
NCBI Description  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir__S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]
```

```
Seq. No.      163996
Seq. ID       LIB3177-070-P1-K1-G4
Method        BLASTX
NCBI GI       g4741960
BLAST score   500
E value       1.0e-50
Match length  116
% identity    84
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

Seq. No.	163997
Seq. ID	LIB3177-070-P1-K1-G5
Method	BLASTN
NCBI GI	g4567237
BLAST score	404
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

```
Seq. No.      163998
Seq. ID      LIB3177-070-P1-K1-G6
Method       BLASTN
NCBI GI      g2749918
BLAST score   215
E value      1.0e-117
Match length  295
% identity    98
NCBI Description Arabidopsis thaliana chromosome I BAC F3I6 genomic
sequence, complete sequence [Arabidopsis thaliana]
```


